10. (Amended) A method for detecting a cellular proliferative disorder associated with CACNA1G, CDX2, EGFR, FBN1, GPR37, HSPA6, IQGAP2, KL, PAR2, PITX2, PTCH, SDC1or SDC4 comprising:

a) contacting a nucleic acid-containing specimen from a subject with an agent that provides a determination of the methylation state of at least one CpG island of a gene or associated regulatory region of the gene;

wherein the gene is selected from the group consisting of APOB, CACNA1G, CDX2, EGFR, FBN1, GPR37, HSPA6, IQGAP2, KL, PAR2, PITX2, PTCH, SDC1, SDC4 and combinations thereof and

b) detecting aberrant methylation of a region of the gene or regulatory region, wherein hypermethylation of a region as compared to the same region of the gene or associated regulatory region in a subject not having said cellular proliferative disorder is indicative of a cellular proliferative disorder.